

## SEQUENCE LISTING

<110> Zuker, Charles S. The Regents of the University of California <120> Assays for Sensory Modulators Using a Sensory Cell Specific G-Protein Alpha Subunit <130> 02307E-092610US <140> US 09/492,028 <141> 2000-01-26 <150> US 60/117,367 <151> 1999-01-27 <160> 14 <170> PatentIn Ver. 2.1 <210> 1 <211> 1503 <212> DNA <213> Mus sp. <220> <221> CDS <222> (157)..(1224) <223> mouse taste cell specific G-protein alpha 14 subunit (TC-Galpha14) <400> 1 aactgccttc gagaagcgtt agcctagaga tccgagcctc ttctccatac catagttggt 60 tcaggtggtt tcctcttcaa accttgcgtc tgcggataat ccgcgcggcc gggcgttaag 120 ctccaqqtcc ctqtcqctcc gtcgaggtgg caagcc atg gcc ggc tgc tgc tgt Met Ala Gly Cys Cys Cys ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag 222 Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln 40 atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc 366 Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly 55 60 ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg 414 Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met 85 75 80

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Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu 115 120 125

Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu 130 135 140

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- Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys 355 360 365
- His Ala Phe Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met 370 375 380
- Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly 385 390 395 400
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- Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly 435 440 445
- Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
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- Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser 485 490 495
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- Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe 515 520 525
- Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu 530 535 540
- Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe 545 550 555 560

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Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln 645 650 655

Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
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Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser 675 680 685

Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro 690 695 700

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Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn 725 730 735

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Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr 785 790 795 800

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Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu 100 105 110

Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp 115 120 125

Lys Tyr Gln Val Glu Thr Met Val Leu Leu Gln Lys Phe Gly Trp 130 135 140

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Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val 195 200 205

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Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala 225 230 235 240

Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met 245 250 255

Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala 260 265 270

Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys 275 280 285

His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln 290 295 300

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- Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys 805 810 815
- Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn 820 825 830
- Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser 835 840

- <210> 13
- <211> 843
- <212> PRT
- <213> Mus sp.

<220>

<223> mouse G-protein coupled receptor (GPCR) B4 amino acid sequence

<400> 13

Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu His

1 10 15

Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu 20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu 50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe 65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu 85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu 115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro 130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe 145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp 165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His 180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp 195 200 205

Ile Val Val Leu Val Ser Asp Asp Tyr Gly Arg Glu Asn Ser His 210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe 225 230 235 240

Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu 245 250 255

Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser 260 265 270

- Ala Arg Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe 275 280 285
- Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala 290 295 300
- Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu 305 310 315 320
- Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile 325 330 335
- Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg 340 345 350
- Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp 355 360 365
- Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser 370 375 380
- Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala 385 390 395 400
- His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys 405 410 415
- Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn 420 425 430
- Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met 435 440 445
- Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn 450 455 460
- Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr 465 470 475 480
- Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile 485 490 495
- Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile 500 505 510
- Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr
  515 520 525
- Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly 530 535 540
- Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu 545 550 555
- Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu 565 570 575
- Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp 580 585 590

Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys 595 600 605

Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val 610 615 620

Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe 625 630 635 640

Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser 645 650 655

Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala 660 665 670

Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe 675 680 685

Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr 690 695 700

Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile
705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val 740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met 770 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr 785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys 805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn 820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser 835 840

<210> 14

<211> 669

<212> PRT

<213> Homo sapiens

<220>

<223> human G-protein coupled receptor (GPCR) B4 amino acid sequence

<400> 14

Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg Phe
1 5 10 15

- Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu Ala
  20 25 30
- Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val Leu 35 40 45
- Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly Glu
  50 60
- Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu Pro 65 70 75 80
- Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg Leu
  85 90 95
- Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
  100 105 110
- Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val Leu 115 120 125
- Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp Ala 130 135 140
- Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly Thr
  145 150 155 160
- Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser Glu 165 170 175
- Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg Thr 180 185 190
- Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn Ala 195 200 205
- Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val Val 210 215 220
- Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His Ser 225 230 235 240
- Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr Pro 245 250 255
- Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu Asp
  260 265 270
- His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu Glu 275 280 285
- Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser Val 290 295 300
- Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Lys Thr Ser 305 310 315 320
- Leu His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser Lys Arg 325 330 335

- Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val Cys Cys 340 345 350
- Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His Thr Glu 355 360 365
- Cys Pro Asn Asn Glu Trp Ser Tyr Gln Ser Glu Thr Ser Cys Phe Lys 370 375 380
- Arg Gln Leu Val Phe Leu Glu Trp His Glu Ala Pro Thr Ile Ala Val 385 390 395 400
- Ala Leu Leu Ala Ala Leu Gly Phe Leu Ser Thr Leu Ala Ile Leu Val 405 410 415
- Ile Phe Trp Arg His Phe Gln Thr Pro Ile Val Arg Ser Ala Gly Gly 420 425 430
- Pro Met Cys Phe Leu Met Leu Thr Leu Leu Leu Val Ala Tyr Met Val
  435
  440
  445
- Val Pro Val Tyr Val Gly Pro Pro Lys Val Ser Thr Cys Leu Cys Arg 450 455 460
- Gln Ala Leu Phe Pro Leu Cys Phe Thr Ile Cys Ile Ser Cys Ile Ala 465 470 475 480
- Val Arg Ser Phe Gln Ile Val Cys Ala Phe Lys Met Ala Ser Arg Phe 485 490 495
- Pro Arg Ala Tyr Ser Tyr Trp Val Arg Tyr Gln Gly Pro Tyr Val Ser 500 505 510
- Met Ala Phe Ile Thr Val Leu Lys Met Val Ile Val Val Ile Gly Met 515 520 525
- Leu Ala Arg Pro Gln Ser His Pro Arg Thr Asp Pro Asp Pro Lys 530 535 540
- Ile Thr Ile Val Ser Cys Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe 545 550 555 560
- Asn Thr Ser Leu Asp Leu Leu Leu Ser Val Val Gly Phe Ser Phe Ala 565 570 575
- Tyr Met Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile 580 585 590
- Thr Leu Ser Met Thr Phe Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr 595 600 605
- Phe Met Ser Ala Tyr Ser Gly Val Leu Val Thr Ile Val Asp Leu Leu 610 620
- Val Thr Val Leu Asn Leu Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro 625 630 635 640

Lys Cys Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr 645  $\phantom{0}655$ 

Phe Asn Ser Met Ile Gln Gly Tyr Thr Met Arg Arg Asp 660 665